CLAIMS

1/ Sequence of nucleotides coding for at least a part of the N-terminal region of a polypeptide specifically toxic towards larvae of the Lepidoptera of the family of the Noctuidae, and preferably towards S.littoralis, characterized by its capacity of hybridization with a gene capable of expressing a polypeptide toxic towards larvae of S.littoralis.

2/ Sequence of nucleotides of about 3 kb corresponding to the HindIII-PstI restriction fragment derived from B.thuringiensis capable of hybridizing with the probes 1, 2, 3 of pHTA2 reported in figure 2.

3/ Sequence according to Claim 1 or 2, characterized in that it contains in the following order the sites :
HindIII - HincII - BglII - KpnI - HindIII - PstI.

4/ Sequence of nucleotides according to any one of the Claims 1 to 3, characterized in that it is obtained in vitro from a single strain of B.thuringiensis.

5/ Sequence of nucleotides according to Claim 4, characterized in that the strain of B.thuringiensis is the aizawai 7-29 strain.

6/ Sequence of nucleotides according to any one of the Claims 1 to 3, characterized in that it is obtained by in vitro genetic recombination of DNA sequences from two different strains of B.thuringiensis.

7/ Sequence according to Claim 6, characterized in that the 2 strains of B.thuringiensis correspond to the strains entomocidus 6-01 and aizawai 7-29, respectively.

8/ Sequence of nucleotides, characterized in that it codes for a polypeptide capable of forming an immunological complex with antibodies directed against polypeptides with a larvicidal activity towards S.littoralis.

9/ Sequence of nucleotides characterized in that it has the capacity to hybridize with a probe formed from the sequence (I) exhibiting the following chain arrangement :

52
GTC TAC TTG ACA GGG GTA GGA ACA TAA TCG GTC AAT TTT AAA TAT GGG GCA TAT ATT GAT
112
ATT TTA TAA AAT TTG TTA CGT TTT TTG TAT TTT TTC ATA AGA TGT GTC ATA TGT ATT AAA
172
TCC TGG TAA TGA AAA ACA GTA TCA AAC TAT CAG AAC TTT GGT AGT TTA ATA AAA AAA CGG
232
AGG TAT TTT ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT AAT
292
CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT TCA TCA ATT GAT ATT
352
TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC TTT GTA CCA GGG GGA GGA TTT TTA GTT
412
GGA TTA ATA GAT TTT GTA TGG GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA
472
CAA ATT GAA CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT GCT
532
AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA TTT AAA GAA TGG GAA
592
GAA GAT CCT AAT AAT CCA GAA ACC AGG ACC AGA GTA ATT GAT GGC TTT CGT ATA CTT GAT
652
GGG CTA CTT GAA AGG GAC ATT CCT TCG TTT CGA ATT TCT GGA TTT GAA GTA CCC CTT TTA
712
TCC GTT TAT GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT TTT
772
GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT AAT AGA CTA ATT AGG
832
CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT ACG TAT AAT CGG GGA TTA AAT AAT TTA
892
CCC AAA TCT ACG TAT CAA GAT TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG
952
ACT GTA TTA GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC

or from the sequence (III) exhibiting the following chain arrangement :

```
1
GAG CTT CAA TAG AAT CTC AAA TCT CGA TGA CTG CTT AGT CTT TTT AAT ACT GTC TAC TTG ACA GGG GTA GAA ACA TAA TCG GTC AAT TTT
 31
AAA TAT GGG GCA TAT AAT TTA TAA AAT TTG TTA CGT TTT TTG TAT TTT TTC ATA AGA TGT GTC ATA TGT ATT AAA TCG TGG TAA
 61
TCA AAA ACA GTA TCA AAC TAT CAG AAC TTT GGT AGT TTA ATA AAA AAA CGG AGG TAT TTT ATG GAG GAA AAT AAT CAA TGC ATA
 91
CCT TAC AAT TGT TTA AGT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT TCA TCA ATT GAT TCT CTG TCA
121
CTT GTT CAG TTT CTG GTA TCA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG GGA ATA GTT GGC CCT TCT
151
CAA TGG GAT GCA TTT CTA GTA CAA ATT CAA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT GCT AAT TTA GAA
181
GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG AAA GCA TTT AAA GAA TGG GAA GAA GAT CCT AAT AAT CCA GCA ACC AGG ACC AGA GTA ATT
211
GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT CCT TCG TTT CGA ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT
241
GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA
271
AAC TAT AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT ACG TAT AAT CGG GCA TTA AAT AAT TTA CCG AAA TCT
301
ACG TAT CAA GAT TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC
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991
AAT AGG AGA TAT CCA ATT CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT AAT TTT AAT CCA CAG TTA CAG TCT
1081
GTA GCT CAA TTA CCT ACT TTT AAC GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG AAT AAT CTT ACA ATC TTT
1171
ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC ATA ACA TCT CCT
1261
ATA TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA ATT CCT ACT TTA CGA
1351
TTA TTA CAG CAA CCT TGC CAG CGC CAC CAT TTT AAT TTA CGT GGT GGT GAA GGA GTA GAA TTT TCT ACA CCT ACA AAT AGC TTT ACG TAT
1441
CGA GGA AGA GGT ACG GTT GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT AAT AGT GTG CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT
1531
CAT GCA ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GAT GTA GTA TTT TCT TGG ACG CAT CAT AGT GCA ACT CTT ACA AAT
1621
ACA ATT GAT CCA GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT
1711
ACA GGA GGG GAT ATC CTT CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT TCA CCA ATT ACC CAA AGA TAC CGT
1801
TTA AGA TTT CGT TAC GCT TCC AGT AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG GGA GGC CAA GTT AGT GTA

1691

GAT AIG CCT CTT CAG AAA ACT ATG GAA AIA GGG GAG AAC TIA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT CCT TTT TCA TTT
1981

AGA GCT AAT CCA GAT ATA ATT GGG AIA AGT GAA CAA CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT AIA GAT AAA ATT
2071

GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT TTA GAA AGA GCA CAA AAG GCG GIG AAT GCC CTG TTT ACT TCT TCC AAT
2161

CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT
2251

GAA AAG CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC
2341

AAT AGA CAA CCA GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA
2431

CCG GGT ACC GTT GAT GAG TGC TAT CCA ACG TAT TTA TAT CAG AAA AIA GAT GAG TCG AAA TTA AAA GCT TAT ACC CGT TAT GAA TTA AGA
2521

GGG TAT ATC GAA GAT AGT CAA GAC TTA GAA ATC TAT TTG ATC GCG TAC AAT GCA AAA CAC GAA ATA GTA AAT GTG CCA GGC ACG GGT TCC
2611

TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT CCT GAT CTA GAT
2701

TGT TCC TGC AG

10/ Sequence of nucleotides coding for a polypeptide toxic specifically towards larvae of the Lepidoptera of the family of the Noctuidae, and preferably towards S.littoralis, characterized in that it includes the chain arrangement (I) or (III) defined in Claim 9.

11/ Sequence of nucleotides according to Claim 9 or 10, characterized in that it has an ATG initiation codon situated at position 241.

12/ Sequence according to any one of the Claims 9 to 11, characterized by a GGAGG binding site to ribosomes at positions 230 to 234.

13/ Sequence according to one of the Claims 10 to 12, characterized in that it contains the sequence included between the nucleotides at position 137 and 177 (position -103 to -63) upstream from the ATG initiation codon) which is homologous to the extent of about at least 70% with the region present upstream from the gene for the crystal of the strain kurstaki-HD1 Dipel (BTK) which contains the three promoters BtI, BtII and Ec, functional in B.thuringiensis and E.coli, respectively.

14/ Sequence of nucleotides, characterized in that it codes for a polypeptide comprising the sequence of amino acids (II) below :

MET GLU GLU ASN ASN GLN ASN GLN CYS ILE PRO TYR ASN CYS LEU SER ASN
PRO GLU GLU VAL LEU LEU ASP GLY GLU ARG ILE SER THR GLY ASN SER SER ILE ASP ILE
SER LEU SER LEU VAL GLN PHE LEU VAL SER ASN PHE VAL PRO GLY GLY GLY PHE LEU VAL
GLY LEU ILE ASP PHE VAL TRP GLY ILE VAL GLY PRO SER GLN TRP ASP ALA PHE LEU VAL
GLN ILE GLU GLN LEU ILE ASN GLU ARG ILE ALA GLU PHE ALA ARG ASN ALA ALA ILE ALA
ASN LEU GLU GLY LEU GLY ASN ASN PHE ASN ILE TYR VAL GLU ALA PHE LYS GLU TRP GLU
GLU ASP PRO ASN ASN PRO GLU THR ARG THR ARG VAL ILE ASP ARG PHE ARG ILE LEU ASP
GLY LEU LEU GLU ARG ASP ILE PRO SER PHE ARG ILE SER GLY PHE GLU VAL PRO LEU LEU
SER VAL TYR ALA GLN ALA ALA ASN LEU HIS LEU ALA ILE LEU ARG ASP SER VAL ILE PHE
GLY GLU ARG TRP GLY LEU THR THR ILE ASN VAL ASN GLU ASN TYR ASN ARG LEU ILE ARG
HIS ILE ASP GLU TYR ALA ASP HIS CYS ALA ASN THR TYR ASN ARG GLY LEU ASN ASN LEU
PRO LYS SER THR TYR GLN ASP TRP ILE THR TYR ASN ARG LEU ARG ARG ASP LEU THR LEU
THR VAL LEU ASP ILE ALA ALA PHE PRO ASN TYR ASP

or that it codes for a polypeptide comprising the sequence of amino acids (IV) below:

MET GLU GLU ASN ASN GLN ASN GLN CYS ILE

271
PRO TYR ASN CYS LEU SER ASN PRO GLU GLU VAL LEU LEU ASP GLY GLU ARG ILE SER THR GLY ASN SER SER ILE ASP ILE SER LEU SER

361
LEU VAL GLN PHE LEU VAL SER ASN PHE VAL PRO GLY GLY GLY PHE LEU VAL GLY LEU ILE ASP PHE VAL TRP GLY ILE VAL GLY PRO SER

451
GLN TRP ASP ALA PHE LEU VAL GLN ILE GLU GLN LEU ILE ASN GLU ARG ILE ALA GLU PHE ALA ARG ASN ALA ALA ILE ALA ASN LEU GLU

541
GLY LEU GLY ASN ASN PHE ASN ILE TYR VAL GLU ALA PHE LYS GLU TRP GLU GLU ASP PRO ASN ASN PRO ALA THR ARG THR ARG VAL ILE

631
ASP ARG PHE ARG ILE LEU ASP GLY LEU GLU ARG ASP ILE PRO SER PHE ARG ILE SER GLY PHE GLU VAL PRO LEU LEU SER VAL TYR

721
ALA GLN ALA ALA ASN LEU HIS LEU ALA ILE LEU ARG ASP SER VAL ILE PHE GLY GLU ARG TRP GLY LEU THR THR ILE ASN VAL ASN GLU

811
ASN TYR ASN ARG LEU ILE ARG HIS ILE ASP GLU TYR ALA ASP HIS CYS ALA ASN THR TYR ASN ARG GLY LEU ASN ASN LEU PRO LYS SER

901
THR TYR GLN ASP TRP ILE THR TYR ASN ARG ARG ASP LEU THR LEU THR VAL LEU ASP ILE ALA ALA PHE PHE PRO ASN TYR ASP

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  991
ASN ARG ARG TYR PRO ILE GLN PRO VAL GLY GLN LEU THR ARG GLU VAL TYR THR ASP PRO LEU ILE ASN PHE ASN PRO GLN LEU GLN SER
 1081
VAL ALA GLN LEU PRO THR PHE ASN VAL MET GLU SER SER ALA ILE ARG ASN PRO HIS LEU PHE ASP ILE LEU ASN ASN LEU THR ILE PHE
 1171
THR ASP TRP PHE SER VAL GLY ARG ASN PHE TYR TRP GLY GLY HIS ARG VAL ILE SER SER LEU ILE GLY GLY GLY ASN ILE THR SER PRO
 1261
ILE TYR GLY ARG GLU ALA ASN GLN GLU PRO PRO ARG SER PHE THR PHE ASN GLY PRO VAL PHE ARG THR LEU SER ILE PRO THR LEU ARG
 1351
LEU LEU GLN GLN PRO CYS GLN ARG HIS HIS PHE ASN LEU ARG GLY GLY GLU GLY VAL GLU PHE SER THR PRO THR ASN SER PHE THR TYR
 1441
ARG GLY ARG GLY THR VAL ASP SER LEU THR GLU LEU PRO PRO GLU ASP ASN SER VAL PRO PRO ARG GLU GLY TYR SER HIS ARG LEU CYS
 1531
HIS ALA THR PHE VAL GLN ARG SER GLY THR PRO PHE LEU THR THR GLY VAL VAL PHE SER TRP THR HIS ARG SER ALA THR LEU THR ASN
 1621
THR ILE ASP PRO GLU ARG ILE ASN GLN ILE PRO LEU VAL LYS GLY PHE ARG VAL TRP GLY GLY THR SER VAL ILE THR GLY PRO GLY PHE
 1711
THR GLY GLY ASP ILE LEU ARG ARG ASN THR PHE GLY ASP PHE VAL SER LEU GLN VAL ASN ILE ASN SER PRO ILE THR GLN ARG TYR ARG
 1801
LEU ARG PHE ARG TYR ALA SER SER ARG ASP ALA ARG VAL ILE VAL LEU THR GLY ALA ALA SER THR GLY VAL GLY GLY GLN VAL SER VAL
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 151
ASN MET PRO LEU GLN LYS THR MET GLU ILE GLY,GLU ASN LEU THR SER ARG THR PHE ARG TYR THR ASP PHE SER.ASN PRO PHE SER PHE
 301
ARG ALA ASN PRO ASP ILE ILE GLY ILE SER GLU GLN PRO LEU PHE GLY ALA GLY SER ILE SER SER GLY GLU LEU TYR ILE ASP LYS ILE
 451
GLU ILE ILE LEU ALA ASP ALA THR PHE GLU ALA·GLU SER ASP LEU GLU ARG ALA GLN LYS ALA VAL ASN ALA LEU PHE THR SER SER ASN
 601
GLN ILE GLY LEU LYS THR ASP VAL THR ASP TYR·HIS ILE ASP GLN VAL SER ASN LEU VAL ASP CYS LEU SER ASP GLU PHE CYS LEU ASP
 751
GLU LYS ARG GLU LEU SER GLU LYS VAL LYS HIS ALA LYS ARG LEU SER ASP·GLU ARG ASN LEU LEU GLN ASP PRO ASN PHE ARG GLY ILE
 901
ASN ARG GLN PRO ASP ARG GLY TRP ARG GLY SER THR ASP ILE THR ILE GLN GLY GLY ASP ASP VAL PHE LYS GLU ASN TYR VAL THR LEU
1051
PRO GLY THR VAL ASP GLU CYS TYR PRO THR TYR LEU TYR GLN LYS ILE ASP GLU SER LYS LEU LYS ALA TYR THR ARG TYR GLU LEU ARG
1201
GLY TYR ILE GLU ASP SER GLN ASP LEU GLU ILE TYR LEU ILE ARG TYR ASN ALA LYS HIS GLU ILE VAL ASN VAL PRO GLY THR GLY SER
1351
LEU TRP PRO LEU SER ALA GLN SER PRO ILE GLY LYS CYS GLY GLU PRO ASN ARG CYS ALA PRO HIS LEU GLU TRP ASN PRO ASP LEU ASP
1501
CYS SER CYS
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15/ Recombinant expression and cloning vector containing at least a part of the nucleotide sequence such as defined in any one of the Claims 1 to 14.

16/ Plasmid according to Claim 15 characterized in that it is pHT671 as represented in figure 4, or pHT71 comprising a HindIII-PstI DNA fragment constituted uniquely of DNA derived from the aizawai 7-29 strain.

17/ Modified bacterial strains, characterized in that after transformation they contain a sequence of nucleotides according to one of the Claims 1 to 14.

18/ Bacterial strain according to Claim 17, characterized in that it contains at least one recombinant vector according to Claim 15 or 16.

19/ Polypeptide toxic towards larvae of the Lepidoptera and preferentially towards S.littoralis, characterized in that it is capable of forming an immunological complex with antibodies directed against polypeptides with larvicidal activity towards S.littoralis.

20/ Polypeptide according to Claim 19, characterized in that it contains the sequence (II) or the sequence (IV) of amino acids defined in Claim 14.

21/ Procedure for obtaining a nucleotide sequence coding for at least a part of the N-terminal region of a polypeptide toxic specifically towards larvae of the Lepidoptera of the family of the Noctuidae, and preferentially towards S.littoralis, characterized by the following steps :

- the carrying out of a hybridization between a sequence of nucleotides from a strain of B.thuringiensis active against S.littoralis, on the one hand, and, on the other, one or several sequences of nucleotides utilized as probes derived from the 5' part of a restriction fragment of a gene for a δ-endotoxin of B.thuringiensis, this part coding for the N-terminal part of a polypeptide toxic towards the Lepidoptera, and derived from the 3' part of this fragment coding for the COOH part of the polypeptide,
- the isolation of the fragment,
- its cloning in a vector, followed by its purification.

22/ Procedure according to Claim 21, characterized in that the hybridization probes utilized are obtained from a gene for a δ-endotoxin derived from a aizawai 7-29 strain coding for a protein of 130kDa active against P.brassicae and inactive towards S.littoralis, this gene having been cloned in the recombinant plasmid pHTA2.

23/ Procedure according to Claim 21 or 22, characterized in that the fragment recombined with the vector in the cloning step is elaborated from at least one sequence of nucleotides derived from at least one recombinant vector containing a sequence of nucleotides from at least one strain of B.thuringiensis.

24/ Procedure according to Claim 23, characterized in that the fragment recombined with the vector in the cloning step is elaborated from several sequences of nucleotides derived from recombinant vectors containing sequences of nucleotides from at least 2 different strains of B.thuringiensis, possessing the same restriction maps and themselves containing all or part of the sequences of nucleotides capable of coding for a polypeptide active preferentially towards S.littoralis.

25/ Procedure according to Claim 23, characterized in that the fragment recombined with the vector in the cloning step is elaborated from a HindIII-PstI restriction fragment derived from the aizawai 7-29 strain.

26/ Procedure according to Claim 24, characterized in that the fragment recombined with the vector in the cloning step is elaborated from a HindIII-HincII restriction fragment derived from the entomocidus 6-01 strain and from a HincII-PstI restriction fragment derived from the aizawai 7-29 strain.

27/ Procedure according to Claim 22, characterized in that the restriction fragment recombined according to Claim 25 is carried preferentially by a plasmid pHTA6 and the restriction fragments recombined according to Claim 26, HindIII-HincII and HincII-PstI, are carried preferentially by the respective recombinant plasmids pHTE6 and pHTA6, the said plasmids pHTA6 and pHTE6 being those isolated with the aid of a probe constituted by a PvuII fragment of 2 kb of the plasmid pBT15-88 corresponding to the internal part of a gene for the chromosomal crystal of the berliner 1715 strain, from

transforming clones containing nucleotide sequences derived from B.thuringiensis strains active towards larvae of the Lepidoptera, inter-alia S.littoralis.

28/ Larvicidal composition with preferential activity towards S.littoralis, characterized in that it contains an efficacious amount of polypeptide such as defined in any one of the Claims 19 to 20 expressed by the nucleotide sequences according to any one of the Claims 1 to 14, the vector according to the Claim 15, or the plasmid according to the Claim 16, or the bacterial strain according to any one of the Claims 17 or 18.

29/ Application of the nucleotide sequences according to any one of the Claims 1 to 14 to produce a polypeptide toxic towards Lepidoptera, and preferentially S.littoralis, in microorganisms capable of expressing recombinant vectors containing these sequences such as E.coli, B.subtilis, B.cereus or B.thuringiensis.

30/ Application according to Claim 29, characterized in that the sequences of nucleotides are introduced into microorganisms living in the environment or in association with the plants such as Pseudomonas, Azospirillum or Rhizobium and capable of expressing recombinant vectors containing these sequences.

31/ Application according to Claim 29 or 30, characterized in that the nucleotide sequences are introduced into microorganisms in combination with different δ-endotoxin genes.

32/ Application of the nucleotide sequences according to any one of the Claims 1 to 14 to the transformation of plants sensitive to S.littoralis, characterized in that it comprises the transfer and the expression of these sequences in these plants.

33/ Plant cells, the genome of which, after transformation by means of a non-essentially biological procedure, possesses in a stable manner a sequence of nucleotides capable of expressing a polypeptide toxic towards S.littoralis, such as defined in any one of the Claims 1 to 14 and cells derived from their division.

34/ Plants having in particular S.littoralis as predator, transformed by a non-essentially biological procedure, the genome of which possesses in a stable manner a sequence of nucleotides such

as defined in any one of the Claims 1 to 14, capable of expressing a polypeptide toxic towards S.littoralis and plants derived from their reproduction, their multiplication, or hybrid crosses.

35/ Plant having in particular S.littoralis as predator, possessing in addition to their initial phenotypic and genotypic characters the property of expressing a polypeptide toxic preferentially towards S.littoralis, this property resulting from the insertion in its genome by genetic manipulation of a sequence of nucleotides capable of expressing the said polypeptide.

36/ Seed capable of giving rise to a plant according to Claim 34 or 35 or derived from such a plant, characterized in that it has integrated into its genome, by genetic manipulation, a sequence of nucleotides according to any one of the Claims 1 to 14.